

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/672,074A  
Source: JPW16  
Date Processed by STIC: 5-1-06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 05/01/2006

PATENT APPLICATION: US/10/672,074A

TIME: 13:00:18

Input Set : A:\DC-293.ReplacmntSeq.txt

Output Set : N:\CRF4\05012006\J672074A.raw

3 &lt;110&gt; APPLICANT: Sundstrom, Paula

5 &lt;120&gt; TITLE OF INVENTION: Methods for Regulating Bud-Hypha Transitions and cAMP Levels

in

6 Candida albicans

8 &lt;130&gt; FILE REFERENCE: 48544-00012 (DC-0293)

10 &lt;140&gt; CURRENT APPLICATION NUMBER: US 10/672,074A

11 &lt;141&gt; CURRENT FILING DATE: 2003-09-29

13 &lt;150&gt; PRIOR APPLICATION NUMBER: US 09/801,774

14 &lt;151&gt; PRIOR FILING DATE: 2001-03-09

16 &lt;160&gt; NUMBER OF SEQ ID NOS: 29

18 &lt;170&gt; SOFTWARE: PatentIn version 3.3

20 &lt;210&gt; SEQ ID NO: 1

21 &lt;211&gt; LENGTH: 545

22 &lt;212&gt; TYPE: PRT

23 &lt;213&gt; ORGANISM: Candida albicans

25 &lt;400&gt; SEQUENCE: 1

27 Met Ser Thr Glu Glu Ser Gln Phe Asn Val Gln Gly Tyr Asn Ile Ile

28 1 5 10 15

31 Thr Ile Leu Lys Arg Leu Glu Ala Ala Thr Ser Arg Leu Glu Asp Ile

32 20 25 30

35 Thr Ile Phe Gln Glu Glu Ala Asn Lys Asn His Tyr Gly Val Asp Ser

36 35 40 45

39 Leu Thr Glu Lys Gly Thr Pro Lys Ser Arg Thr Val Glu Ser Ser Glu

40 50 55 60

43 Ala Thr Ser Asp Gly Lys Ser Leu Glu Ser Thr Ser Phe Ala Thr Phe

44 65 70 75 80

47 Ser Glu Ala Pro Val Glu Lys Ser Lys Leu Ile Val Glu Phe Glu Asn

48 85 90 95

51 Phe Val Glu Ser Tyr Val His Pro Leu Val Glu Thr Ser Lys Lys Ile

52 100 105 110

55 Asp Ser Leu Val Gly Glu Ser Ala Gln Tyr Phe Tyr Glu Ala Phe Val

56 115 120 125

59 Glu Gln Gly Lys Phe Leu Glu Leu Val Leu Gln Ser Gln Gln Pro Asp

60 130 135 140

63 Met Thr Asp Pro Ala Leu Ala Lys Ala Leu Glu Pro Met Asn Ala Lys

64 145 150 155 160

67 Cys Thr Lys Ile Asn Glu Leu Lys Asp Ser Asn Arg Lys Ser Pro Phe

68 165 170 175

71 Phe Asn His Leu Ser Thr Phe Ser Glu Ser Asn Ala Val Phe Tyr Trp

72 180 185 190

75 Ile Gly Ile Pro Thr Pro Val Ser Tyr Ile Thr Asp Thr Lys Asp Thr

76 195 200 205

79 Val Lys Phe Trp Ser Asp Arg Val Leu Lys Glu Tyr Lys Thr Lys Asp

80 210 215 220

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83 Gln Val His Val Glu Trp Val Lys Gln Thr Leu Ser Val Phe Asp Glu
84 225                230                235                240
87 Leu Lys Asn Tyr Val Lys Glu Tyr His Thr Thr Gly Val Ala Trp Asn
88                245                250                255
91 Pro Lys Gly Lys Pro Phe Ala Glu Val Val Ser Gln Gln Thr Glu Ser
92                260                265                270
95 Ala Ala Lys Asn Ser Ser Ser Ala Ser Gly Ser Ala Gly Gly Ala Ala
96                275                280                285
99 Pro Pro Pro Pro Pro Pro Pro Pro Pro Ala Thr Phe Phe Asp Asp Thr
100                290                295                300
103 Glu Lys Asp Ser Glu Asn Pro Ser Pro Ala Ser Gly Gly Ile Asn Ala
104 305                310                315                320
107 Val Phe Ala Glu Leu Asn Gln Gly Ala Asn Ile Thr Ser Gly Leu Lys
108                325                330                335
111 Lys Val Asp Lys Ser Glu Met Thr His Lys Asn Pro Glu Leu Arg Lys
112                340                345                350
115 Gln Pro Pro Val Ala Pro Lys Lys Pro Ala Pro Pro Lys Lys Pro Ser
116                355                360                365
119 Ser Leu Ser Gly Gly Val Ser Ser Ala Pro Val Lys Lys Pro Ala Lys
120                370                375                380
123 Lys Glu Leu Ile Asp Gly Thr Lys Trp Ile Ile Gln Asn Phe Thr Lys
124 385                390                395                400
127 Ala Asp Ile Ser Asp Leu Ser Pro Ile Thr Ile Glu Val Glu Met His
128                405                410                415
131 Gln Ser Val Phe Ile Gly Asn Cys Ser Asp Val Thr Ile Gln Leu Lys
132                420                425                430
135 Gly Lys Ala Asn Ala Val Ser Val Ser Glu Thr Lys Asn Val Ala Leu
136                435                440                445
139 Val Ile Asp Ser Leu Ile Ser Gly Val Asp Val Ile Lys Ser Tyr Lys
140                450                455                460
143 Phe Gly Ile Gln Val Leu Gly Leu Val Pro Met Leu Ser Ile Asp Lys
144 465                470                475                480
147 Ser Asp Glu Gly Thr Ile Tyr Leu Ser Gln Glu Ser Ile Asp Asn Asp
148                485                490                495
151 Ser Gln Val Phe Thr Ser Ser Thr Thr Ala Leu Asn Ile Asn Ala Pro
152                500                505                510
155 Lys Glu Asn Asp Asp Tyr Glu Glu Leu Ala Val Pro Glu Gln Phe Val
156                515                520                525
159 Ser Lys Val Val Asn Gly Lys Leu Val Thr Gln Ile Val Glu His Ala
160                530                535                540

```

163 Gly

164 545

167 &lt;210&gt; SEQ ID NO: 2

168 &lt;211&gt; LENGTH: 1634

169 &lt;212&gt; TYPE: DNA

170 &lt;213&gt; ORGANISM: Candida albicans

172 &lt;400&gt; SEQUENCE: 2

173 atgtcaaccg aggagagtca attcaatgtt caaggttaca atattatcac aatcttgaaa 60

175 agattagagg cagcaacgtc tcgtcttgag gacattacca ttttccaaga ggaagcaaac 120

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177 aaaaaccaca tggagttgat tctctcactg aaaaggggaac ccccaaaagc agaactgttg 180
179 aatcgtcaga agcaacttcc gatggtaa at cactcgaatc tacatcattt gccacttttt 240
181 ctgaagctcc tgtagaaaaa tccaaattga ttgtggaatt tgagaacttt gttgaaagct 300
183 acgttcatcc acttgttgaa acatccaaaa agatcgattc cttggtgggg gagtccgccc 360
185 aatattttta tgaggcattt gtcgaacaag ggaaattttt ggagcttgta ttgcaatccc 420
187 aacaaccaga tatgactgat ccagctttgg caaaggcatt agaaccaatg aatgctaaat 480
189 gcaccaaaaat taacgaattt aaaaattccaa tcgtaaatct ccattcttca atcatttaag 540
191 cacttttcagt gaaagtaatg ccgtttttta ttggattggg atccctacac cagtctcgta 600
193 cattactgat actaaagata cagtcaaatt ttggtctgac agagttttaa aagaatacaa 660
195 gaccaaagac caagtgcag ttgaatgggt aaaacaaaca ttatctgttt ttgacgaatt 720
197 gaagaattat gttaaagaat atcacacaac tgggtgtgct tggaaccca aaggaaagcc 780
199 ttttgcagaa gttgtatctc agcaaacaga gagtgtgct aagaattctt cgtctgcttc 840
201 tggttctgca ggaggagcag ctccaccacc acctccacct ccacctccag caacgttttt 900
203 tgatgacact gaaaaagaca gtgaaaatcc atctcagctt caggtggtat taatgcggtt 960
205 ttgctgaatt gaatcaagg tccaacatca catctggttt aaaaaaagtc gacaaatctg 1020
207 agatgacgca taagaaccct gaattaagaa aacagccacc agttgcacca aaaaaaccag 1080
209 cccccccaaa gaagccatct agtttatccg gtggtgtgag ttcagctcca gtaaagaagc 1140
211 ctgctaagaa ggagttgatt gacggtacaa aatggataat tcaaaatttt acaaaagctg 1200
213 atatttccga ttgagtccta attaccattg aagttgagat gcatcaatct gttttcattg 1260
215 gtaattgtag tgatgtcacc attcagttga aaggtaaagc aaatgcagtg tcggtatcgg 1320
217 aacacaagaa tgtggctctt gtcattgatt cgttgatttc cggagtcgat gttattaaat 1380
219 cctacaagtt tggatatacaa gttttagggt tggtaaccaat gttgagtatt gataaatcag 1440
221 atgaaggac tatctatttg tcgcaagaaa gcattgacaa tgatagtcag gtttttacta 1500
223 gtagcactac agcactcaac atcaatgcac caaaggaaaa tgatgattat gaagaattgg 1560
225 ctgttcttga acaatttggt agtaagggtg tgaatggcaa attagtcact caaattgttg 1620
227 aacatgctgg ataa 1634

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230 &lt;210&gt; SEQ ID NO: 3

231 &lt;211&gt; LENGTH: 150

232 &lt;212&gt; TYPE: PRT

233 &lt;213&gt; ORGANISM: Candida albicans

235 &lt;400&gt; SEQUENCE: 3

```

237 Asn Pro Ile Gln Thr Leu Gly Leu Leu Val Ala Ala Leu Gly His Asp
238 1 5 10 15
241 Val Gly His Pro Gly Thr Thr Asn Asp Phe Met Ile Lys Phe Ser Ala
242 20 25 30
245 Pro Thr Ala Leu Leu Tyr Asn Asp Arg Ser Val Leu Glu Ser Tyr His
246 35 40 45
249 Ala Ser Leu Phe Ile Asn Lys Val Leu Arg Ile Cys Trp Pro Asp Leu
250 50 55 60
253 Leu Thr Cys Thr Ile Glu Glu Lys Ser Glu Leu Thr Ile Arg Ser Leu
254 65 70 75 80
257 Ile Ile Ser Ser Ile Leu Ala Thr Asp Met Gly Glu His Asn Glu Tyr
258 85 90 95
261 Val Asn Arg Leu Lys Ser Phe Lys Thr His Asn Glu Ile Leu Asn His
262 100 105 110
265 Asp Asn Thr Val Lys Leu Ile Ser Ala Leu Leu Ile Lys Cys Ala Asp
266 115 120 125
269 Ile Ser Asn Val Thr Arg Pro Leu Arg Val Ser Ala Gln Trp Ala Met
270 130 135 140

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273 Val Leu Ser Arg Glu Phe
274 145                      150
277 <210> SEQ ID NO: 4
278 <211> LENGTH: 135
279 <212> TYPE: PRT
280 <213> ORGANISM: Saccharomyces cerevisiae
282 <400> SEQUENCE: 4
284 Asn Pro Val Gln Thr Leu Leu Leu Cys Met Ala Ala Ile Gly His Asp
285 1                      5                      10                      15
288 Val Gly His Pro Gly Thr Asn Asn Gln Leu Leu Cys Asn Cys Glu Ser
289                      20                      25                      30
292 Glu Val Ala Gln Asn Phe Lys Asn Val Ser Ile Leu Glu Asn Phe His
293                      35                      40                      45
296 Arg Glu Leu Phe Gln Gln Leu Leu Ser Glu His Trp Pro Gln Leu Leu
297 50                      55                      60
300 Ser Ile Ser Lys Lys Lys Phe Asp Phe Ile Ser Glu Ala Ile Leu Ala
301 65                      70                      75                      80
304 Thr Asp Met Ala Leu His Ser Gln Tyr Glu Asp Arg Leu Met His Glu
305                      85                      90                      95
308 Asn Pro Met Lys Gln Ile Thr Leu Ile Ser Leu Ile Ile Lys Ala Ala
309                      100                     105                     110
312 Asp Ile Ser Asn Val Thr Arg Thr Leu Ser Ile Ser Ala Arg Trp Ala
313                      115                     120                     125
316 Tyr Leu Ile Thr Leu Glu Phe
317 130                      135
320 <210> SEQ ID NO: 5
321 <211> LENGTH: 149
322 <212> TYPE: PRT
323 <213> ORGANISM: Homo sapiens
325 <400> SEQUENCE: 5
327 Glu Asp Ile Glu Ile Phe Ala Leu Phe Ile Ser Cys Met Cys His Asp
328 1                      5                      10                      15
331 Leu Asp His Arg Gly Thr Asn Asn Ser Phe Gln Val Ala Ser Lys Ser
332                      20                      25                      30
335 Val Leu Ala Ala Leu Tyr Ser Ser Glu Gly Ser Val Met Glu Arg His
336                      35                      40                      45
339 His Phe Ala Gln Ala Ile Ala Ile Leu Asn Thr His Gly Cys Asn Ile
340 50                      55                      60
343 Phe Asp His Phe Ser Arg Lys Asp Tyr Gln Arg Met Leu Asp Leu Met
344 65                      70                      75                      80
347 Arg Asp Ile Ile Leu Ala Thr Asp Leu Ala His His Leu Arg Ile Phe
348                      85                      90                      95
351 Lys Asp Leu Gln Lys Met Ala Glu Val Gly Tyr Asp Arg Asn Asn Lys
352                      100                     105                     110
355 Gln His His Arg Leu Leu Leu Cys Leu Leu Met Thr Ser Cys Asp Leu
356                      115                     120                     125
359 Ser Asp Gln Thr Lys Gly Trp Lys Thr Thr Arg Lys Ile Ala Glu Leu
360 130                      135                      140
363 Ile Tyr Lys Glu Phe

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Input Set : A:\DC-293.ReplacmntSeq.txt

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364 145

367 &lt;210&gt; SEQ ID NO: 6

368 &lt;211&gt; LENGTH: 22

369 &lt;212&gt; TYPE: DNA

370 &lt;213&gt; ORGANISM: Artificial Sequence

372 &lt;220&gt; FEATURE:

373 &lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

375 &lt;400&gt; SEQUENCE: 6

376 gcaaataaat ccgtaggaaa cg

22

379 &lt;210&gt; SEQ ID NO: 7

380 &lt;211&gt; LENGTH: 20

381 &lt;212&gt; TYPE: DNA

382 &lt;213&gt; ORGANISM: Artificial Sequence

384 &lt;220&gt; FEATURE:

385 &lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

387 &lt;400&gt; SEQUENCE: 7

388 ccaccaacac caacagaaaa

20

391 &lt;210&gt; SEQ ID NO: 8

392 &lt;211&gt; LENGTH: 566

393 &lt;212&gt; TYPE: PRT

394 &lt;213&gt; ORGANISM: Candida albicans

396 &lt;400&gt; SEQUENCE: 8

398 Met Ala Glu Val Leu Ser Leu Val Asp Leu Glu Ile Pro Gln Val Thr

399 1 5 10 15

402 Asp Lys Tyr Tyr Lys Phe Asp Thr Phe Lys His Leu Ile Cys His Leu

403 20 25 30

406 Phe Lys Lys Thr Ser Thr Glu Thr Asp Ser Asn Val Pro Ile Val Ile

407 35 40 45

410 Ile Phe Pro Thr Asn Asn Asp Ile Pro Ser Arg Lys Thr Arg Ser Thr

411 50 55 60

414 Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Asn Thr Ser Lys Leu Asp

415 65 70 75 80

418 Asn Leu Pro Phe Ser Asp Lys Ser Leu Leu Ile Gln Phe Phe Phe Thr

419 85 90 95

422 His Leu Asn Ile Leu Met Ile Gln Gly Glu Asn Ser Asp Glu Gly Lys

423 100 105 110

426 Leu Tyr Gln Glu Ile Ser Ser Ala Lys Glu Leu Leu Thr Asn Arg Ile

427 115 120 125

430 Ser Arg Val Gly Asn Trp Thr Gly Thr Thr His Phe Arg Tyr Cys Arg

431 130 135 140

434 His Glu Asn Asp Cys Gly Leu Leu Asn Gln His Ser Lys Ile Ala Gly

435 145 150 155 160

438 Ile Ile Pro Thr Met Thr Tyr Ile Leu Asn Cys Asn Ala Thr Arg Ser

439 165 170 175

442 Glu Ile Ala Thr Asn Gln Leu Ile Tyr Leu Tyr Arg Leu Met Ile Glu

443 180 185 190

446 Glu Ile Asn Phe Ile Glu Leu Leu Gln Asp Ala Ser Thr Thr Arg Leu

447 195 200 205

450 Ser Gln Leu Cys Tyr Ala Val Gly His Trp Ser Phe Pro Ala His Asn

**VERIFICATION SUMMARY**

DATE: 05/01/2006

PATENT APPLICATION: US/10/672,074A

TIME: 13:00:19

Input Set : A:\DC-293.ReplacmntSeq.txt

Output Set: N:\CRF4\05012006\J672074A.raw